



substituteseq.txt

SEQUENCE LISTING

<110> Kiselev, Vsevolod I
Petr, Sveshnikov G

<120> METHODS, KITS, AND COMPOSITIONS FOR THE DEVELOPMENT AND USE
OF MONOCLONAL ANTIBODIES SPECIFIC TO ANTIGENS TRADITIONALLY
OF LOW IMMUNOGENICITY

<130> Immunize

<150> RU 2003128660
<151> 2003-09-25

<160> 22

<170> PatentIn version 3.1

<210> 1
<211> 309
<212> DNA
<213> Human papillomavirus type 16

<220>
<221> CDS
<222> (7)..(303)
<223>

<400> 1

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| Ile Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu | |
| 1 5 10 | |
| gat ttg caa cca gag aca act gat ctc tac tgt tat gag caa tta aat | 96 |
| Asp Leu Gln Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn | |
| 15 20 25 30 | |
| gac agc tca gag gag gat gaa ata gat ggt cca gct gga caa gca | 144 |
| Asp Ser Ser Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala | |
| 35 40 45 | |
| gaa ccg gac aga gcc cat tac aat att gta acc ttt tgt tgc aag tgt | 192 |
| Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys | |
| 50 55 60 | |
| gac tct acg ctt cgg ttg tgc gta caa agc aca cac gta gac att cgt | 240 |
| Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg | |
| 65 70 75 | |
| act ttg gaa gac ctg tta atg ggc aca cta gga att gtg tgc ccc atc | 288 |
| Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile | |
| 80 85 90 | |
| tgt tct cag aaa cca ggatcc | 309 |
| Cys Ser Gln Lys Pro | |
| 95 | |

<210> 2
<211> 99
<212> PRT

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<213> Human papillomavirus type 16

<400> 2

Ile Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu
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Gln Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser
20 25 30
Ser Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro
35 40 45
Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser
50 55 60
Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu
65 70 75 80
Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser
85 90 95
Gln Lys Pro

<210> 3

<211> 330

<212> DNA

<213> Human papillomavirus type 18

<220>

<221> CDS

<222> (7)..(324)

<223>

<400> 3

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| Ser Met His Gly Pro Lys Ala Thr Leu Gln Asp Ile Val Leu | |
| 1 5 10 | |
| cat tta gag ccc caa aat gaa att ccg gtt gac ctt cta tgt cac gag | 96 |
| His Leu Glu Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys His Glu | |
| 15 20 25 30 | |
| caa tta agc gac tca gag gaa aac gat gaa ata gat gga gtt aat | 144 |
| Gln Leu Ser Asp Ser Glu Glu Asn Asp Glu Ile Asp Gly Val Asn | |
| 35 40 45 | |
| cat caa cat tta cca gcc cga cga gct gaa cca caa cgt cac aca atg | 192 |
| His Gln His Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met | |
| 50 55 60 | |
| ttg tgt atg tgt tgt aag tgt gaa gcc aga att gag cta gta gta gaa | 240 |
| Leu Cys Met Cys Cys Lys Cys Glu Ala Arg Ile Glu Leu Val Val Glu | |
| 65 70 75 | |
| agc tca gca gac gac ctt cga gca ttc cag cag ctg ttt ctg aac acc | 288 |
| Ser Ser Ala Asp Asp Leu Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr | |
| 80 85 90 | |
| ctg tcc ttt gtg tgt ccg tgg tgt gca tcc cag cag ggatcc | 330 |
| Leu Ser Phe Val Cys Pro Trp Cys Ala Ser Gln Gln | |

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95

100

105

<210> 4
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<212> PRT
<213> Human papillomavirus type 18

<400> 4

Ser Met His Gly Pro Lys Ala Thr Leu Gln Asp Ile Val Leu His Leu
1 5 10 15

Glu Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys His Glu Gln Leu
20 25 30

Ser Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln
35 40 45

His Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met Leu Cys
50 55 60

Met Cys Cys Lys Cys Glu Ala Arg Ile Glu Leu Val Val Glu Ser Ser
65 70 75 80

Ala Asp Asp Leu Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr Leu Ser
85 90 95

Phe Val Cys Pro Trp Cys Ala Ser Gln Gln
100 105

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<211> 5321
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of recombinant vector pQE30-dnak

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attgtgagcg gataacaatt tcacacagaa ttcattaaag aggagaaatt aactatgaga 120
ggatcgcac accatcacca tcacggatcc gctcgtgcgg tcgggatcga cctcgggacc 180
accaactccg tcgtctcggt tctggaaggt ggcgaccggg tcgtcgtcgc caactccgag 240
ggctccagga ccacccggtc aattgtcgcg ttcgcccgc acggtgaggt gctggtcggc 300
cagcccgcca agaaccaggc agtgaccaac gtcgatcgca ccgtgcgc ggtcaagcga 360
cacatgggca gcgactggtc catagagatt gacggcaaga aatacaccgc gccggagatc 420
agcgcccgca ttctgtatgaa gctgaagcgc gacgcccagg cctacacctgg tgaggacatt 480
accgacgcgg ttatcacgac gccccctac ttcaatgacg cccagcgtca ggccaccaag 540
gacgcccggcc agatcgccgg cctcaacgtg ctgcggatcg tcaacgagcc gaccgcggcc 600
gcgctggcct acggcctcga caagggcgag aaggagcgcg gaatcctggt cttcgacttg 660

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| | | | | | | |
|-------------|-------------|------------|------------|-------------|-------------|------|
| ggtgtggca | cttcgacgt | ttccctgctg | gagatcggcg | agggtgtgg | tgaggtccgt | 720 |
| gccacttcgg | gtgacaacca | cctcggcggc | gacgactggg | accagcgggt | cgtcgattgg | 780 |
| ctgggtggaca | agttcaaggg | caccagcggc | atcgatctga | ccaaggacaa | gatggcgatg | 840 |
| cagcggctgc | ggaagccgc | cgagaaggca | aagatcgagc | tgagttcgag | tcagtcacc | 900 |
| tcgatcaacc | tgccctacat | caccgtcgac | gccgacaaga | acccttgcgtt | tttagacgag | 960 |
| cagctgaccc | gcgcggagtt | ccaacggatc | actcaggacc | tgctggaccg | cactcgcaag | 1020 |
| ccgttccagt | cgtgtatcgc | tgacaccggc | atttcggtgt | cggagatcga | tcacgttgc | 1080 |
| ctcgtgggtg | gttcgacccg | gatgcccgcg | gtgaccgatc | tggtcaagga | actcaccggc | 1140 |
| ggcaaggaac | ccaacaaggg | cgtcaacccc | gatgagggtt | tcgcgggtgg | agccgctctg | 1200 |
| caggccggcg | tcctcaaggg | cgaggtgaaa | gacgttctgc | tgcttgcgtt | taccccgctg | 1260 |
| agcctgggta | tcgagaccaa | gggcgggggt | atgaccaggc | tcatcgagcg | caacaccacg | 1320 |
| atccccacca | agcggtcgga | gactttcacc | accgcccacg | acaaccaacc | gtcggtgccag | 1380 |
| atccaggtct | atcaggggga | gcgtgagatc | gccgcgcaca | acaagttgc | cgggtccctc | 1440 |
| gagctgaccg | gcatcccgcc | ggcgccgcgg | gggattccgc | agatcgaggt | cactttcgac | 1500 |
| atcgacgcca | acggcattgt | gcacgtcacc | gccaaggaca | agggcaccgg | caaggagaac | 1560 |
| acgatccgaa | tccaggaagg | ctcgggcctg | tccaaggaag | acattgaccg | catgatcaag | 1620 |
| gacgccgaag | cgcacgcccga | ggaggatcgc | aagcgtcg | aggaggccga | tgttcgtaat | 1680 |
| caagccgaga | cattggtcta | ccagacggag | aagttcgta | aagaacagcg | tgaggccgag | 1740 |
| ggtgttcga | aggtacctga | agacacgctg | aacaagggtt | atgcccgggt | ggcggaaagcg | 1800 |
| aaggcggcac | ttggcggatc | ggatatttcg | gccatcaagt | cggcgatgga | gaagctgggc | 1860 |
| caggagtcgc | aggctctggg | gcaagcgatc | tacgaagcag | ctcaggctgc | gtcacaggcc | 1920 |
| actggcgctg | cccaccccg | cggcgagccg | ggcgggtccc | acccggctc | ggctgatgac | 1980 |
| gttgtggacg | cggaggtgg | cgacgacggc | cgggaggcca | agtgacggac | gggtcgaccc | 2040 |
| gcagccaagc | ttaattagct | gagcttggac | tcctgttgc | agatccagta | atgacctcag | 2100 |
| aactccatct | ggatttgttc | agaacgctg | gttgcgcgg | ggcgaaaa | attggtgaga | 2160 |
| atccaagcta | gcttggcgag | atttcagga | gctaaggaag | ctaaaatgga | aaaaaaaatc | 2220 |
| actggatata | ccaccgttga | tatatccaa | tggcatcgta | aagaacattt | tgaggcattt | 2280 |
| cagtcagttg | ctcaatgtac | ctataaccag | accgttcagc | tggatattac | ggcctttta | 2340 |
| aagaccgtaa | agaaaaataa | gcacaagttt | tatccggcct | ttattcacat | tcttgcggc | 2400 |
| ctgatgaatg | ctcatccgga | atttcgtatg | gcaatgaaag | acggtgagct | ggtgatatgg | 2460 |
| gatagtgttc | acccttgtta | caccgttttc | catgagcaaa | ctgaaaacgtt | ttcatcgctc | 2520 |

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| tggagtgaat accacgacga | tttccggcag | tttctacaca | tatattcgca | agatgtggcg | 2580 |
| tgttacggtg | aaaacctggc | ctattccct | aaagggtta | ttgagaatat | 2640 |
| tcagccaatc | cctgggtgag | tttcaccagt | tttgattta | acgtggccaa | 2700 |
| ttcttcgccc | ccgtttcac | catggcaaa | tattatacgc | aaggcgacaa | 2760 |
| ccgctggcga | ttcaggttca | tcatgccgtt | tgtgatggct | tccatgtcgg | 2820 |
| aatgaattac | aacagtactg | cgatgagtgg | cagggcgggg | cgttaatttt | 2880 |
| tattggtgcc | cttaaacgccc | tgggttaatg | actctctagc | ttgaggcatac | 2940 |
| aaaggctcag | tcgaaagact | gggccttcg | ttttatctgt | tgttgcgg | 3000 |
| cctgagtagg | acaaatccgc | cctctagagc | tgcctcgcgc | gtttcggtga | 3060 |
| aacctctgac | acatgcagct | cccggagacg | gtcacagctt | gtctgtaaac | 3120 |
| agcagacaag | cccgtcaggg | cgcgtcagcg | ggtgttggcg | ggtgtcgggg | 3180 |
| accagtcac | gtagcgatag | cggagtgtat | actggcttaa | ctatgcggca | 3240 |
| ttgtactgag | agtcgaccat | atgcgggtgt | aaataccgca | cagatgcgt | 3300 |
| accgcacatcg | gcbccttc | gctccctcgc | tcactgactc | gctgcgcctcg | 3360 |
| tgcggcgagc | ggtatcagct | cactcaaagg | cggtaataac | gttatccaca | 3420 |
| ataacgcagg | aaagaacatg | tgagcaaaag | gccagcaaaa | ggccaggaac | 3480 |
| ccgcgttgct | ggcgcccccc | cataggctcc | gccccctga | cgagcatcac | 3540 |
| gctcaagtca | gaggtggcg | aacccgacag | gactataaag | ataccaggcg | 3600 |
| gaagctccct | cgtgcgtct | cctgttccga | ccctgcccgt | taccggatac | 3660 |
| ttctcccttc | gggaagcgt | gchgcttctc | atagctcac | ctgtccgcct | 3720 |
| tgttaggtcg | tcgctccaag | ctgggctgt | tgcacgaacc | ccccgttcag | 3780 |
| gcgccttatac | cggtaactat | cgtcttgagt | ccaacccgt | aagacacgac | 3840 |
| tggcagcagc | cactggtaac | aggattagca | gagcgaggta | tgtaggcggt | 3900 |
| tcttgaagt | gtggcctaac | tacggctaca | ctagaaggac | agtatttgg | 3960 |
| tgctgaagcc | agttaccttc | ggaaaaagag | ttggtagctc | ttgatccggc | 4020 |
| ccgctggtag | cggtggtttt | tttggca | agcagcagat | tacgcgcaga | 4080 |
| ctcaagaaga | tccttgatc | tttctacgg | ggtctgacgc | tcagtggaaac | 4140 |
| gttaaggat | tttggcatg | agattatcaa | aaaggatctt | cacctagatc | 4200 |
| aaaaatgaag | ttttaaatca | atctaaagta | tatatgagta | aacttggtct | 4260 |
| aatgcttaat | cagtgaggca | cctatctcag | cgatctgtct | atttcggtca | 4320 |
| cctgactccc | cgtcgtgtag | ataactacga | tacgggaggg | cttaccatct | 4380 |
| ctgcaatgt | accgcgagac | ccacgctcac | cggctccaga | tttatcagca | 4440 |

substituteseq.txt

| | |
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| cagccggaag ggccgagcgc agaagtggtc ctgcaactt atccgcctcc atccagtc | 4500 |
| ttaattttg ccgggaagct agagtaagta gttcgccagt taatagtttgcgcaacgttgc | 4560 |
| ttgccattgc tacaggcatc gtgggtcac gctgtcggtt tggtatggct tcattcagct | 4620 |
| ccggttccca acgatcaagg cgagttacat gatccccat gtttgcaaa aaagcggttgc | 4680 |
| gctccttcgg tcctccgatc gttgtcagaa gtaagttggc cgcaatgttgc | 4740 |
| ttatggcagc actgcataat tctcttactg tcatgccatc cgtaagatgc ttttctgtga | 4800 |
| ctggtgagta ctcaaccaag tcattctgag aatagtgtat gcccgcaccg agttgctctt | 4860 |
| gcccggcgatc aatacggat aataccgcgc cacatagcag aactttaaaa gtgctcatca | 4920 |
| ttggaaaacg ttcttcgggg cgaaaaactct caaggatctt accgctgttgc | 4980 |
| cgatgttaacc cactcgtgca cccaaactgat cttcagcatc ttttactttc accagcggtt | 5040 |
| ctgggtgagc aaaaacagga aggcaaaatg ccgcaaaaaaaaa gggaaataagg ggcacacggaa | 5100 |
| aatgttgaat actcataactc ttcccttttc aatattatttgc aagcatttttgc cagggttatt | 5160 |
| gtctcatgag cggatacata tttgaatgttgc ttttagaaaaaa taaacaaata ggggttccgc | 5220 |
| gcacatttcc ccgaaaagtgc acacctgacg tctaagaaac cattattatc atgacattaa | 5280 |
| cctataaaaaaa taggcgtatc acgaggccct ttcgtttca c | 5321 |

<210> 6
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<213> Bos taurus

<400> 6

Lys Lys Arg Pro Lys Pro Gly Gly Gly Trp Asn Thr
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<210> 7
<211> 8
<212> PRT
<213> bos taurus

<400> 7

Gln Pro His Gly Gly Gly Trp Gly
1 5

<210> 8
<211> 13
<212> PRT
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<400> 8

Gln Trp Asn Lys Pro Ser Lys Pro Lys Thr Asn Ile Lys
1 5 10

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<210> 9
<211> 17
<212> PRT
<213> bos taurus

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Ile Thr Gln Tyr Gln Arg Glu Ser Gln Ala Tyr Tyr Gln Arg Gly Ala
1 5 10 15

Ser

<210> 10
<211> 19
<212> DNA
<213> Human papillomavirus type 16

<400> 10

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<400> 11

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<210> 13
<211> 20
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<210> 14
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<210> 17
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cttatcgat cctggtttct gagaacagat g 31

<210> 18
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<212> DNA
<213> Artificial sequence

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<223> pHE716 and pHE718 terminal sequences

<220>
<221> misc_feature
<222> (107)..(108)
<223> HSP 16/HSP18 E7 gene insertion site

<400> 18

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ctgaaagtt 130

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<223> Forward primer for pHE716

<400> 19

substituteseq.txt

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| <220> | |
| <223> Reverse primer for pHE718 | |
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10